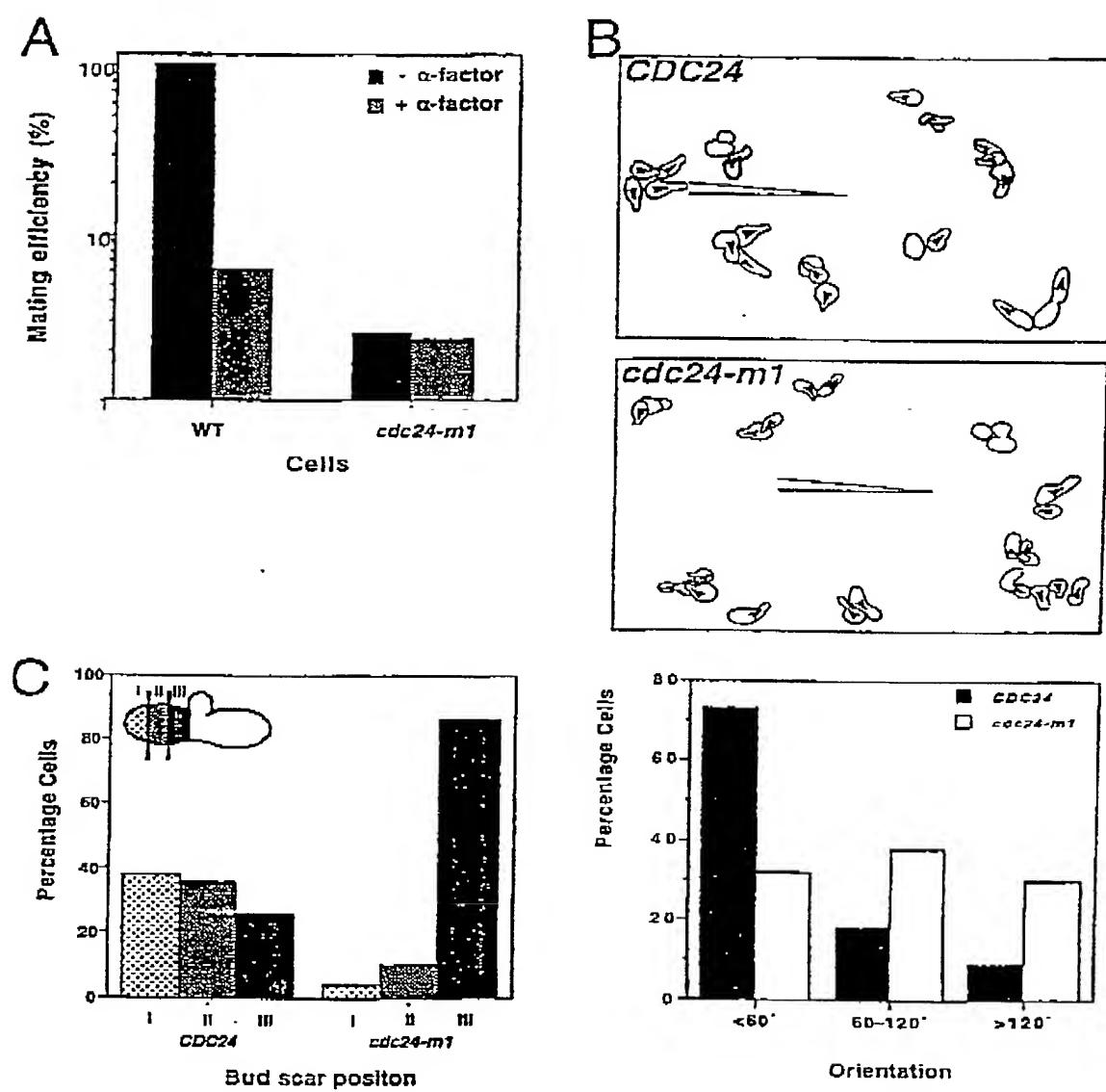
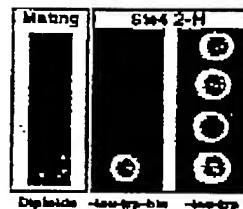
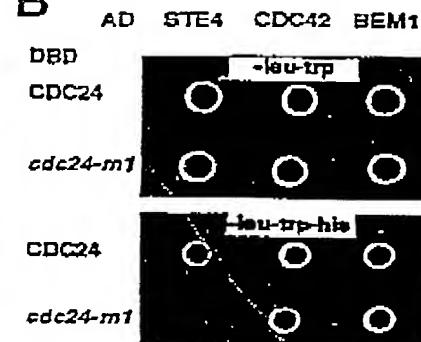
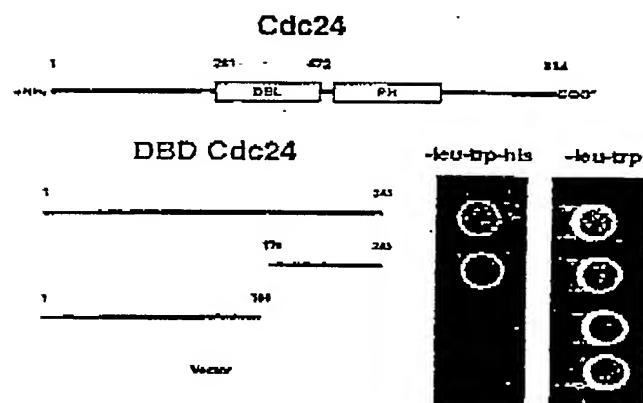
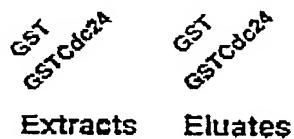
**FIG. 1**

**FIG. 2**

**A**

Cdc24-m1	QFKLPIVIAFDDLRVKRKSI
Cdc24-m2	QFKLPIVIAFGDLRVCKRSI
Cdc24-m3	QFKLPIVIAFDDLRVKRKSI
Ddc24	Se 181 QFKLPIVIAFDDLRVKRKSI 189  +•+   -   +         +     Dd Hu 335 QYEFIDVILSPELKVGKRTI 403

**B****C****D****FIG. 3**

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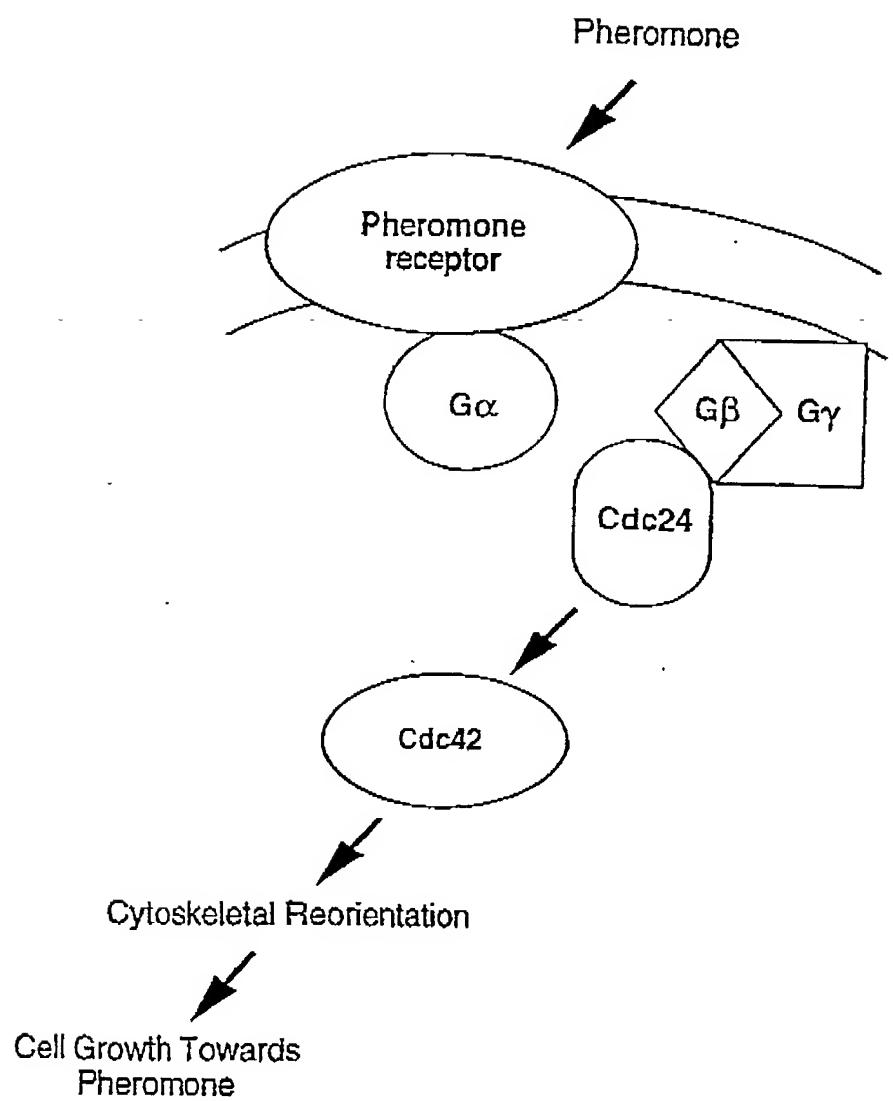


FIG. 4

Figure 5

5  
 2113/1 2143/11  
 ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT  
 M E H P P A A L R T F S T Q S T S S L N  
 2173/21 2203/31  
 TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT  
 S V S T V S S S R I V S S G P V N I N N  
 2233/41 2263/51  
 TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA  
 F N K P S T P K D H L F Y R C E S L K R  
 2293/61 2323/71  
 AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA  
 K L Q K I P G M E P F L N Q A F N Q A E  
 2353/81 2383/91  
 CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT  
 Q L S E Q Q A L A L A Q E R S N G N G H  
 2413/101 2443/111  
 AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC GGT GCC ATG AAT AGA CTT TCA TTG GGT TCT  
 S N G K R H Q S L D G A M N R L S V G S  
 2473/121 2503/131  
 GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT  
 D S S S I Q G S L T R M A T N A S T S S  
 2533/141 2563/151  
 TTA ATC AGT GGT ATG CCA AAC AAC ACT TTA TTT ACG TTT ACT GCA GGG TTG TTA CCA  
 L I S G M P N N N T L F T F T A G V L P  
 2593/161 2623/171  
 GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC  
 A N I S V D P A T H L W K L F Q Q G A P  
 2653/181 2683/191  
 TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT  
 F C V L I N H I L P D S Q I P V V S S D  
 2713/201 2743/211  
 GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG  
 D L R I C K K S V Y D F L I A V K T Q L  
 2773/221 2803/231  
 AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT  
 N F D D E N M F T I S N V F S D N A Q D  
 2833/241 2863/251  
 TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC  
 L I K I I D V I N K L L A E Y S D A S D  
 2893/261 2923/271  
 CTC GGT GGT GGC GAT GAA GAT GTA AAT ATG GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA  
 S G G G D E D V N M D V Q I T D E R S K  
 2953/281 2983/291  
 GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT  
 V F R E I I E T E R K Y V Q D L E L M C  
 3013/301 3043/311  
 AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA ATT TTG TCT TCA GAA CAA ATT CAC TTG TTA  
 K Y R Q D L I E A E N L S S E Q I H L L  
 3073/321 3103/331  
 TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT  
 F P N L N E I I D F Q R R F L N G L E C  
 3133/341 3163/351  
 AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG  
 N I N V P I R Y Q R I G S V F I H A S L  
 3193/361 3223/371  
 GGC CCT TTC AAT GCT TAT GAA CCT TTG ACT ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC  
 G P F N A Y E P W T I G Q L T A I D L I  
 3253/381 3283/391  
 AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT  
 N K E A A N L K K S S S L L D P G F E L  
 3313/401 3343/411  
 CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG  
 Q S Y I L K P I Q R L C K Y P L L K E  
 3373/421 3403/431  
 TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA  
 L I K T S P E Y S K Q D P H G S S S S T  
 3433/441 3463/451  
 TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT  
 S F N E L L V A K T A M K E L A N Q V N

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3493/461  
 GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT  
 E A Q R R A E N I E H L E K L K E R V G  
 3553/481  
 5 AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG  
 N W R G F N L D A Q G E L L F H G Q V G  
 3613/501  
 GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT  
 V K D A E N E K E Y V A Y L F E K I V F  
 10 3673/521  
 TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT  
 F F T E I D D T K K S D K Q E K K S K F  
 3733/541  
 TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA  
 15 S T R K R S T S S N L S S S T T N L L E  
 3793/561  
 TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT  
 S I N N S R K D N T L P L E L K G R V Y  
 20 3853/581  
 ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA  
 I S E I Y N I S A P N T P G S T L I I S  
 3913/601  
 TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA  
 W S G R K E S G S F T L R X R S E E A R  
 25 3973/621  
 AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT  
 N Q W E K C L R D L K T N E M N K Q I H  
 4033/641  
 AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC  
 K K L R D S D S S F N T D D S A I Y D Y  
 4093/661  
 ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG  
 T G I S T S P V N Q S T Q Q Y Y D H R  
 4153/681  
 GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT  
 G S H S S R H H S S S S T L S M M K N N  
 4213/701  
 AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC  
 R V K S G D L S R I S S T S T T L D S F  
 4273/721  
 AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC  
 S N N L N G S P N T T N P S L M S S D A  
 4333/741  
 4363/751  
 ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG  
 T K T I P T F D V A I K L L Y K S T E L  
 4393/761  
 4423/771  
 TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC  
 S E P L I V N A Q I E Y N D L L Q K I I  
 4453/781  
 4483/791  
 50 TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT  
 S Q I I T S N L V A D D V N I S R L R Y  
 4513/801  
 4543/811  
 AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG AAT TCA GAT GAT GAT TCG GGG TTA GTG CTT  
 K D D E G D F V N L N S D D D W G L V L  
 55 4573/821  
 4603/831  
 GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA  
 D M L T S E D F Y Q T S S N E K R S V T  
 4633/841  
 GTG TGG GTT TCT TGA  
 60 V W V S \*

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Figure 6

5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1	MAIQ---TR-FA M R F+	8
C.a. Cdc24p: 1	MEHPPAALRTFSTQ	14
10 S.c. Cdc24p: 9	SGTSLSLDLKPKPSATSISIYPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPOLKPFQLQ	66
	S +SL+ + S+ N+ NKP T +D LF+ C +++++L+ +P ++PFL	
C.a. Cdc24p: 15	STSSLNNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPPLNQ	74
15 S.c. Cdc24p: 67	AYQSSEVLSERQSLLLSQKQHQELLKSNGANRDSSDLAP---TLRSSSISTATSLMSMEG	123
	A+ +E LSE+Q+L L+Q++ SNG S D A + + S S S SL M	
C.a. Cdc24p: 75	AFNQAEOQLSEQQALALAQERSNGNGHSNGKRHQSLDGMNRSLVGSDSSSIQGSLTRMAT	134
20 S.c. Cdc24p: 124	ISYTNNSNPNSATPNMEDTLLTFMSMGILPITMDCDFVTQLSQLFQQGAPLCLIFNSVKPQFK	183
	+ T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +	
C.a. Cdc24p: 135	NASTSSLISCGMPN-NNTLFTFTAGVLPANISVDPATHLWKLFPQQGAPFCVLINHILPDSQ	193
S.c. Cdc24p: 184	LPVIASDDLKVCKKSIYDFILGCKKKHPAFNDEELFTISDVFANSTSQLVKVLEVETLMN	243
	+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K++V+ L+	
25 C.a. Cdc24p: 194	IPVVSSDDLRICKKSVDLIAVKTQLNFDDENMFTISNVFSDNAQDLIKIIDVINKLLA	253
S.c. Cdc24p: 244	SSPTIFFSKSKTQQIMNAENQHRQPQQSSKKHNEYVKIIKEFVATERKYVHDLEILDKY	303
	S + + + + + + E K+ +E + TERKYV DLE++ KY	
C.a. Cdc24p: 254	EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIITERKYVQDLELMCKY	302
30 S.c. Cdc24p: 304	RQQLLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQRIGALFMH-SKHF	362
	RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V QRIG++F+H S	
C.a. Cdc24p: 303	RQDLIEAENLSSEQIHLFPNLNEIIDFQRRFLNGLECNIINVPIRYQRIGSVFIHASLG	362
35 S.c. Cdc24p: 363	FKLYEPWSIGQNAATEFLSSTLHOMRVDESQRFLINNKLELQSFYKPVQRLCRYPLLVK	422
	F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K	
C.a. Cdc24p: 363	FNAYEPWTIGQLTAIDLINKEAANLKKSS--LLDPGFELQSYILKPIQRACKYPLLLK	419
40 S.c. Cdc24p: 423	ELLAE-----SSDDNNNTKELEALDISKNIARSINENQRRTENHQVVKKLYGRV	471
	EL+ SS + EL A K+A +NE QRR EN + ++KL RV	
C.a. Cdc24p: 420	ELIKTSPEYSKQDPHGSSSSTSFnELLVAKTAMKELANQVNEAQRRAEINIELEKLKERV	479
S.c. Cdc24p: 472	VNWKGYRISKPGELLYFDKVFIGTTNNSSEPEREFEVYLFEKILLLFSEVVTKKSASSLI	531
	NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K+	
45 C.a. Cdc24p: 480	GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFEKIVFFFTEIDDTKKSDKQE	535
S.c. Cdc24p: 532	LKKKSSTSASISASNITDNNGSPHHSYHKKRHNSSSSSNNIHLSSSAAIIHSSTNSSDN	591
	K K ST ++SN+ SSS ++ S NS +	
C.a. Cdc24p: 536	KKSFKSTRKRSTSSNL-----SSSTNLLESINNSRKD	568
50 S.c. Cdc24p: 592	NSNNSSSSSLFKL\$ANEPKLDLGRIMIMNLNQIIPQN--NRSINITWESIKEQGNFLK	649
	N+ L+L+GR+ I + I N +L I+W KE G+F L+	
C.a. Cdc24p: 569	NT-----LPLELKGRVYIISBIYNISAPNTPGSTLIISWSGRKESGSFTLR	613
55 S.c. Cdc24p: 650	FKNEETRDNWSSCLQQLIHDLKNEQFKARHSSSTTTSS-----TAKSSSMMSPTTT	701
	+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T	
C.a. Cdc24p: 614	YRSEEARNQWEKCLDLKTNEMNKQIHKKLRSDFSSFTDDSAIYDYGISTSPVNQSTQ	673
S.c. Cdc24p: 702	MNTPNHNSRQT-HDSMASFSSSHMKRVS---DVLPKRRTTSSFESEIKS-----	748
	+H S + H S ++ S RV + TT SF + +	
C.a. Cdc24p: 674	QQYYDHRGSHSSRHSSSSTLSSMMKNNRVRKGDSLRSISSTTLDLFSNNLNGSPNTTNP	733
S.c. Cdc24p: 749	--ISENPKNNSIPESSILFRISYNNNSNNTSSEIFTLLVEKWNFDDLIMAINSKI--SN	804
	+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN	
65 C.a. Cdc24p: 734	SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIIQITSN	787
S.c. Cdc24p: 805	THNNNISPITKIKYQDEDGDFVVLGSDEDWNVAKEMLAENNEKFNLIRLY	854
	++++ I++++Y+D++GDFV L SD+DW + +ML + F +	
C.a. Cdc24p: 788	LVADDVN-ISRLRYKDDEGDFVNLSDDDWGLVLDMLTSED--FYQTSSNEKRSVTWWVS	844

Figure 7a

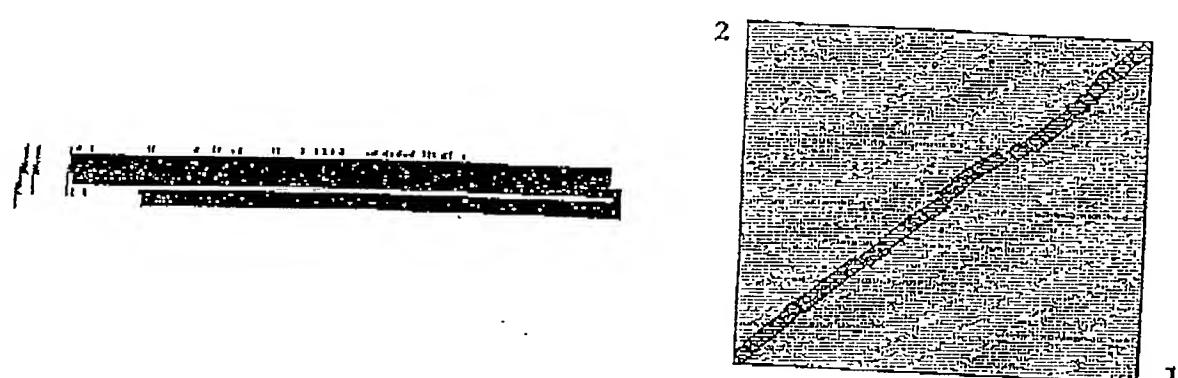
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
x\_dropoff: 50 expect: 10.0 wordsize: 3 Filter Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1-854)

Sequence 2 lcl|C.a. Cdc24p Length 844 (1-844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database.

Score = 446 bits (1136), Expect = e-124  
Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

... (018), Gaps = 112/881 (12%)

Query: 9 SGTSLSDLKPKP SATSISIPMQNV--MNKP VTEQDSL FHICANIRKRLEVL PQLKPF LQL 66  
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL  
Sbjcc: 15 STSSLN SVSTVSSSRIVSSGPVNINNNENKPSL

Query: 67 AYQSSEVLSERQSLLLSQKQHQELLKSNGANRDSSDLAP---TLRSSSISTATSLMSMEG 123  
 Sbjct: 75 A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M  
 AFNQAEQLSEQOQALALAQERSNGNGHSNGKRHQSLDGAMNRISVGSDS

Query: 124 ISYTNSNPSATPNMEDTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKEQFK 183  
           + T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +  
 Sbjct: 135 NASTSSLISGMPPN-NNTLFTFTAGVL PANISVDPATHLWKLFOOCAPCIVL

Query: 184 LPVIASDDLKVCKKSITYDFILGCKKHFAFNDEELFTISDVFANSTSSQLVKLEVVEETLMN 243  
 +PV4+SDDL++CKKS+YDF++ K F+DE +FTIS+VE+++ L+K+++V+ L+  
 Sbjct: 194 IPVVSSDDLICKKSIVYDFLIAVKTQLNPDDENMFTISNVESDNAODI LKLT

Query: 244 SSPTIFPSKSKTQQIMNAENQHRHQPOQQSSKKHNEYVKIIKEFWATERKYVHDLEILDKY 303  
Sbjct: 254 EYSDASDGGGDEDV-----NMDVQITDERSKVFREIITERKYVHDLEILDKY 303

Query: 304 RQQLLDNSNLITSEELYMLFPNLGDAIDFQRRFLISLFINALVEPSKQRIGALFMH-SKHF 362  
 RQ L++- ++SE++++LFPNL + IDFQRRFL LE N V QRIG+F+H S  
 Sbjct: 303 RQDLTEAENLSSEQIHLFPNLNEIIDFQRRFLNGLECNINVPIRYORIGSVELVYLG 362

Query: 363 FKLYEPWSIGQNAAI~~EFLSSTLHKMRVDESQRFIINNKLE~~Q5FLYKPVQR~~LCRYPLL~~VK 422  
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QR~~LC~~C+YPLL+K 422  
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQS~~YILKPIORLC~~KPV~~U~~LIK 418

F Figure 7a cont.

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Query: 423 ELLAE-----SSDDNNNTKELEAALDISKNIARSINENQRRTENHQVVKKLYGRV 471  
 EL+ SS + EL A K +A +NE QRR EN + ++KL RV  
 Sbjct: 420 ELIKTSPEYSKQD?HGSSSSTS?NELLVAKTAMKELANQVNEAQRRRAENTIEHLEKLKERV 479

Query: 472 VNWKGYRISKFGELLYFDKFVISTMNSSSEPEREFEVYLFEKIIILFSEVVTKKSASSLI 531  
 NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +  
 Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV---KDAENEKEYVAYLFEKIVFFTEIDDTKKSDKQE 535

Query: 532 LKKKSSTSASISASANITDNNGSPHYSYHKRHNSSSSNNIHLSSSSAAATIHSSTNSSDN 591  
 K K ST ++SN+ SSS ++ S NS +  
 Sbjct: 536 KKSKF5TRKRSTSSNL-----SSSTNLLESINNSRJD 568

Query: 592 NSNNSSSSSLPKLSANEPKLDLRGRIMIMMNQIIPQN--NRSLNITWESIKEQGNFLLK 649  
 N+ L+L+GR+ I + I N +L I+W KE G+F L+  
 Sbjct: 569 NT-----LPLELKGRVYISEIYNISAPNTPGSTLTISWSGRKESGSPTLR 613

Query: 650 FKNEETRDNWSSCLQQQLIHDLKNEQFKARHHSSTTTSS-----TAKSSSMMSPTTT 701  
 +-+ZE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T  
 Sbjct: 614 YRSEEARQWEKCLRDLKTNEMNKQIHKKLRLDSDSSFTEDDSAIYDYTGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS---DVLPKRRTTSSSFSESEIKS----- 748  
 +H S + H S ++ S RV + TT SF + +  
 Sbjct: 674 QQYYDHRGSHSSRHSSSTLSMMKQNRVKSGDLSRISSTSTLDSPSNNLNGSPNTTNP 733

Query: 749 --ISENFKN SIPESSILFRISYNNNSNNTSSSEIFTLLVEKVWNFDLIMAINSKI--SN 804  
 +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN  
 Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKTIISQIITSN 787

Query: 805 THNNNNTSPITKIKYQDEDGDFVVLGSDEDWNVAKEMLAENN 845  
 +++ I++++Y+D++GDFV L SD+DW + +ML +  
 Sbjct: 788 LVADDVN-ISRLRYKDDEGDFVNLSDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.  
 Gapped Lambda K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 12253  
 Number of Sequences: 0  
 Number of extensions: 709  
 Number of successful extensions: 15  
 Number of sequences better than 10.0: 1  
 Number of HSP's better than 10.0 without gapping: 1  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 1  
 length of query: 844  
 length of database: 90,077,593  
 effective HSP length: 63  
 effective length of query: 781  
 effective length of database: 83353792  
 effective search space: 65099311552  
 effective search space used: 65099311552  
 T: 9  
 A: 40  
 X1: 16 ( 7.2 bits)  
 X2: 128 (49.9 bits)  
 X3: 128 (49.9 bits)  
 S1: 42 (21.9 bits)  
 S2: 73 (32.8 bits)

Figure 7b

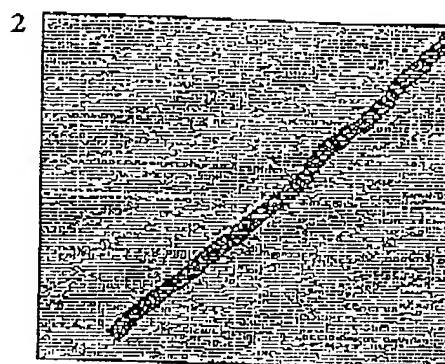
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix  BLOSUM62 gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 Icl|S.c. Cdc24p Length 854 (1 .. 854)

Sequence 2 Icl|S.p. Cdc24p Length 834 (1 .. 834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61  
Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)



Query: 156 DPVTQLSQLFQQGAPLCILFNSVKPQFKLPVIASDDLK---VCKKSITYDFILGCKKKHFAF 212  
DPVT++ + G PLC LEN + + KL V + S L+ VCK S+Y F+L CK  
Sbjct: 67 DPVTEIWLFTRLGYPLCALFNCLPVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSSQLVKLEVETLMNNSPTIFPSKSKTQQIMNAENQERHQPOQS 272  
D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + + + S  
Sbjct: 127 TDAALFSISEIYKPSTAPLVRALQTIELLLKKYEVSNTTKSSTPSPSTDDNVPTGTLNS 186

Query: 273 SKKHNEYVKITKEFVATERKYVADLEILDKYRQQQLDSNLITSEELYMLFPNLGDAIDFQ 332  
++ E TE KY+ DLE L Y L + + + + +F NL + +DFQ  
Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVLQQKQILSQDTILSIFTNLNEILDFQ 244

Query: 333 RRFLISLEINALVEPSKQRIGALFMHSKHFFKLYEPWSIG-QNAAIEFLSSTLHKMRVDE 391  
RRFL+ LE+N + +QR+GALF+ + F +Y+ + NA + + + +V  
Sbjct: 245 RRFLVGLEMNLSLPVEEQLCAGFIALEEGFSVYQVFCTNFPNAQQLIIDNQNQQLKVN 304

Query: 392 SQRFIINNKLELQSFLYKPVQLCRYPLLKELL-AE55DDNNNTKELEAALDISKNTARS 450  
++ EL + L K+P+QR+C+YPLL+ +LL S +EL+ + +A  
Sbjct: 305 ---LLEPSYELPALLIKPIORTCKYPLLLNLQQLKGTPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRTENHQVVKLYGRVVNWKGYRISKFGELLYFDKVPISTTNSSEPEREFEVYL 510  
+NE +R EN + +L RV++WKGY + FG+LL +D V + ++ ERE+ VYL  
Sbjct: 361 VNETRRIHENRNAIIIEQRVIDWKGYSLOQYFGQLLVWDVVNV---CKADIERYHVYL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSAS-----ISASNITDN----- 550  
FEKI++ E+ T K+ A S+ + KK+ S I SNIT  
Sbjct: 417 FEKILLCCKEMSTLKQARSISMNKKTKRLDSLQLKGRILTSNITTVPNHHMGSYAIQI 476

| Figure 7b cont..

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Query: 551 --NGSPHHSYHKRHNSSSNNIHL-----SSAAIIHSSTNSDNNNNSSS 599  
G P H + S+ + +S + I S+ ++ N N SSS  
Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLWKNEHGSFKDIRSAASTPANPVYNRSSS 536  
Query: 600 SLFKLSANEPKLD-LRGRIIMLN--QIIPQNNRSLNITWESIKEQGNFLKFKNEET 655  
K N D LR + N+N I + + +S T + K+ K+ T  
Sbjct: 537 QTSK-GYNSSDYDILLRTHSLDENVNSPTSISSPSSKSSPFTKTTSKDT-----KSATT 588  
Query: 656 RDNWSSCLQQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMSPTTMNT--PNHH 708  
D S +L + R +TST +SSTA S+ + +N+ + +  
Sbjct: 589 TDERPSDFIRLNSEESVGTSLSRTSQTTSTIVSNDSSSTASIPSQISRKISQVNSSLINDYN 648  
Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRRTTSSSFSE 745  
+RQ+H S++ F SSS + + + D + P++ + S+ +S+  
Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708  
Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSEI---FTLLVEKVWNFDDLIMAINSK 801  
+ S+ SS + S N +N + L+V FD+L+ + K  
Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLHEVSLVLUVVAHDITFDELLAKVEHK 768  
Query: 802 IS--NTHNNNISPITKIKYQDEDGDFVVLGSDEDWNVAKE 839  
I + +KY DEDGDF+ + SDED +A E  
Sbjct: 769 IKLCGILKQAVPPRVRALKYVDEDGDFITITSDEDVILMAFE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.  
Gapped  
Lambda K H  
0.270 0.0470 0.230

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 10384  
Number of Sequences: 0  
Number of extensions: 671  
Number of successful extensions: 13  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 2  
Length of query: 834  
Length of database: 90,077,593  
Effective HSP length: 61  
Effective length of query: 773  
Effective length of database: 83489227  
Effective search space: 64537172471  
Effective search space used: 64537172471  
T: 9  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 128 (49.9 bits)  
X3: 128 (49.9 bits)  
Y1: 41 (21.7 bits)  
Y2: 73 (32.8 bits)

Figure 8

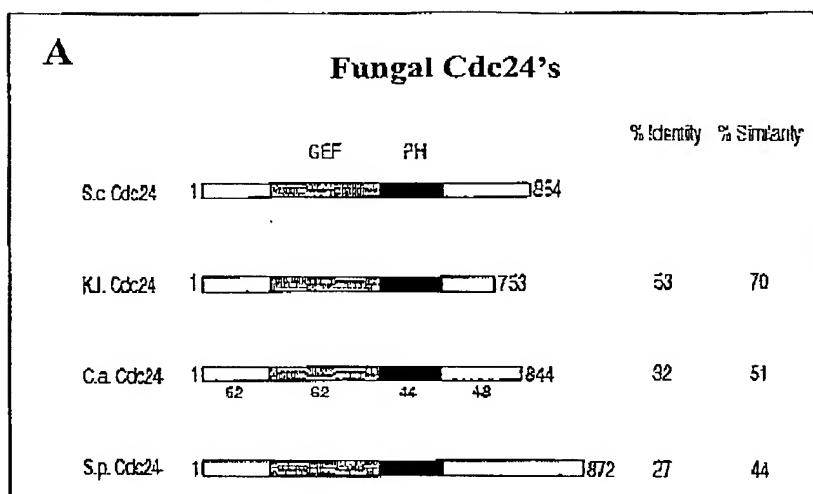
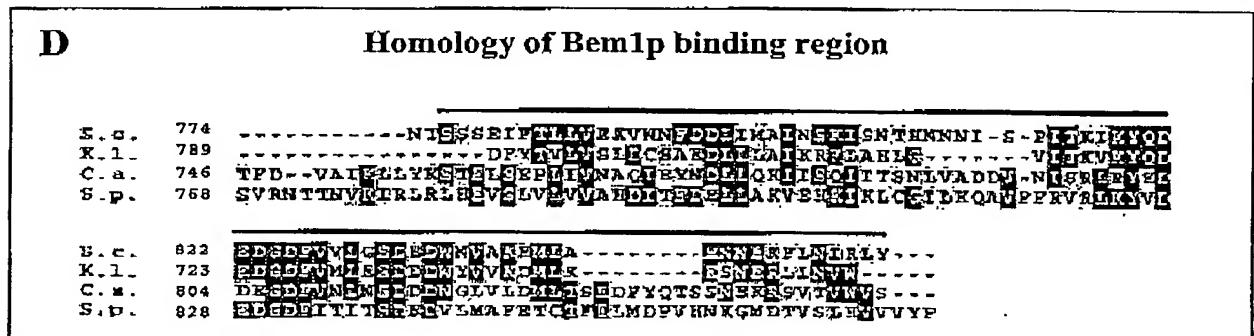
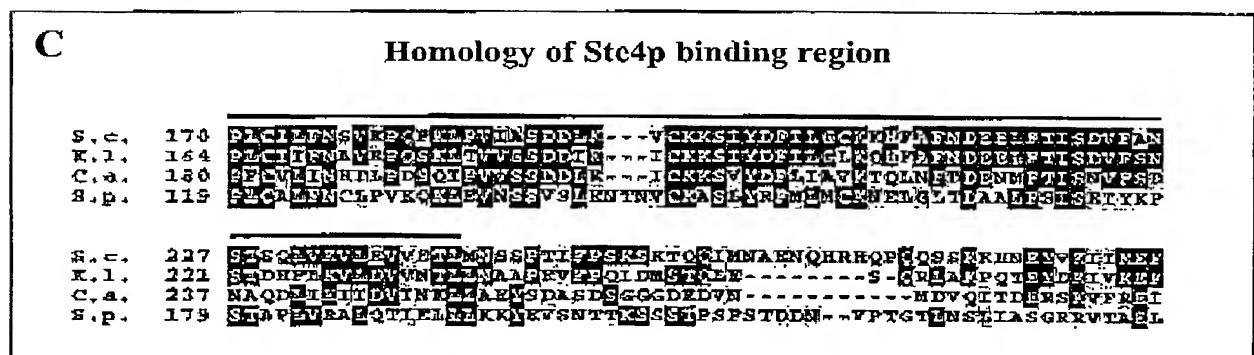
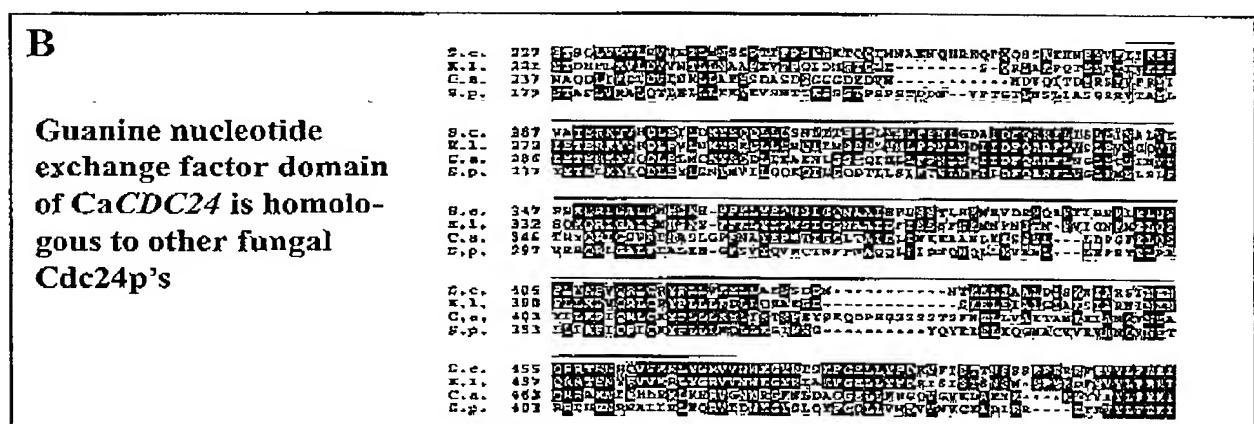
5 Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLICKKSVYDFLI (SEQ ID No 26)

10 Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

**figure 9**

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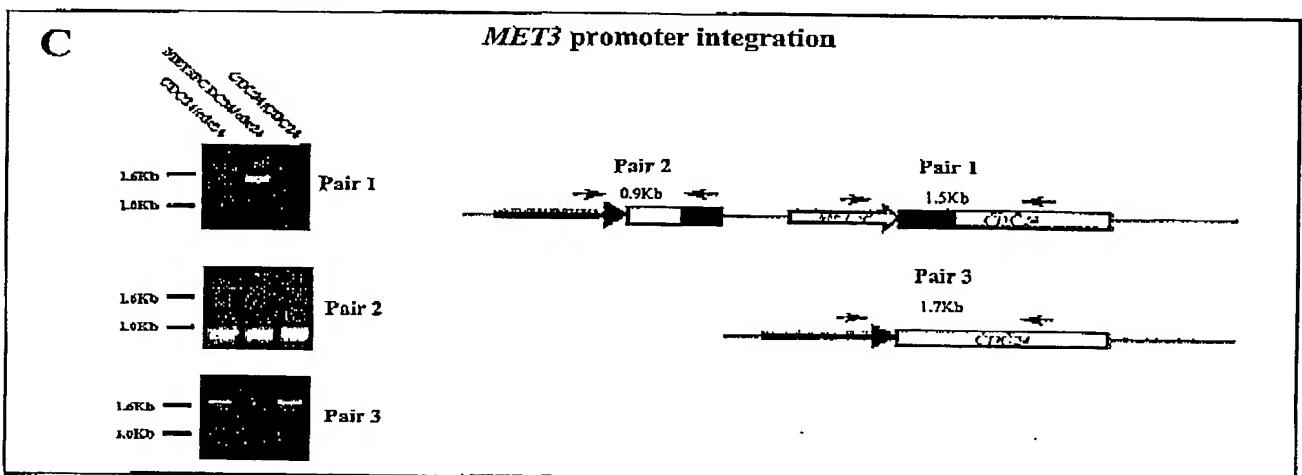
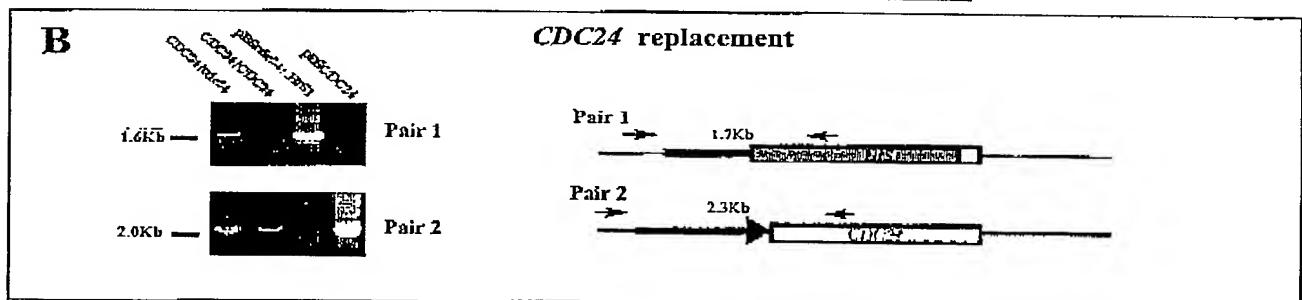
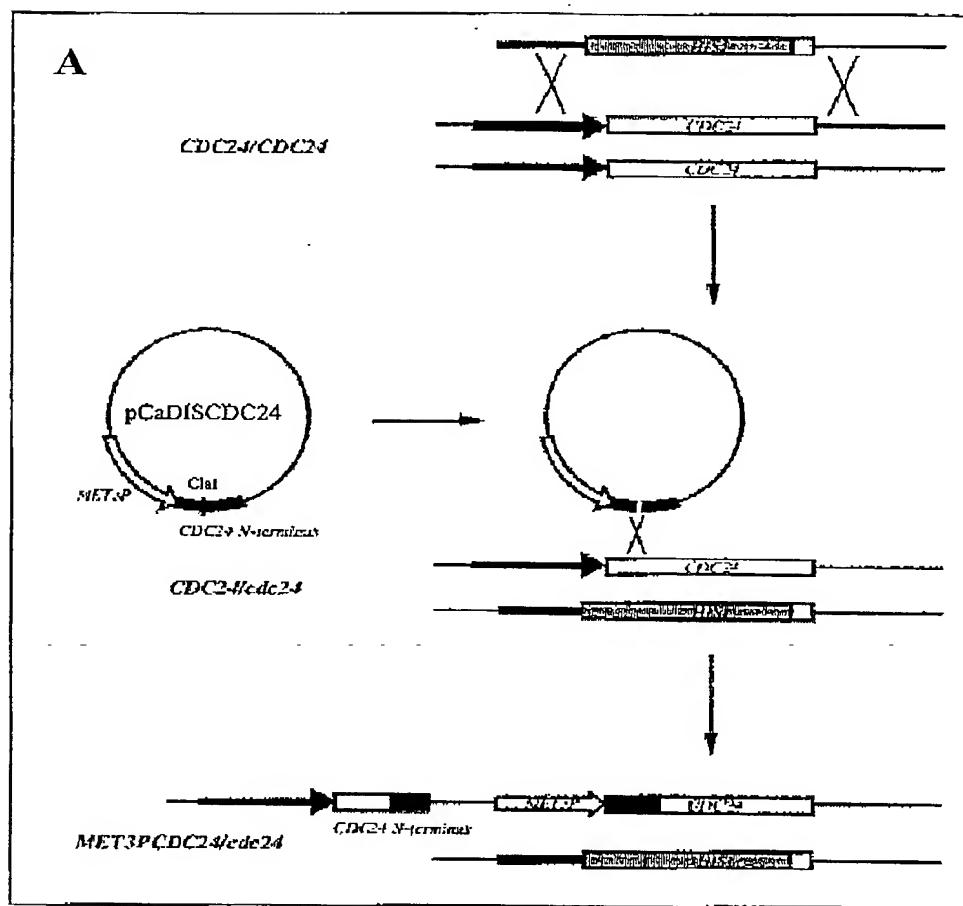
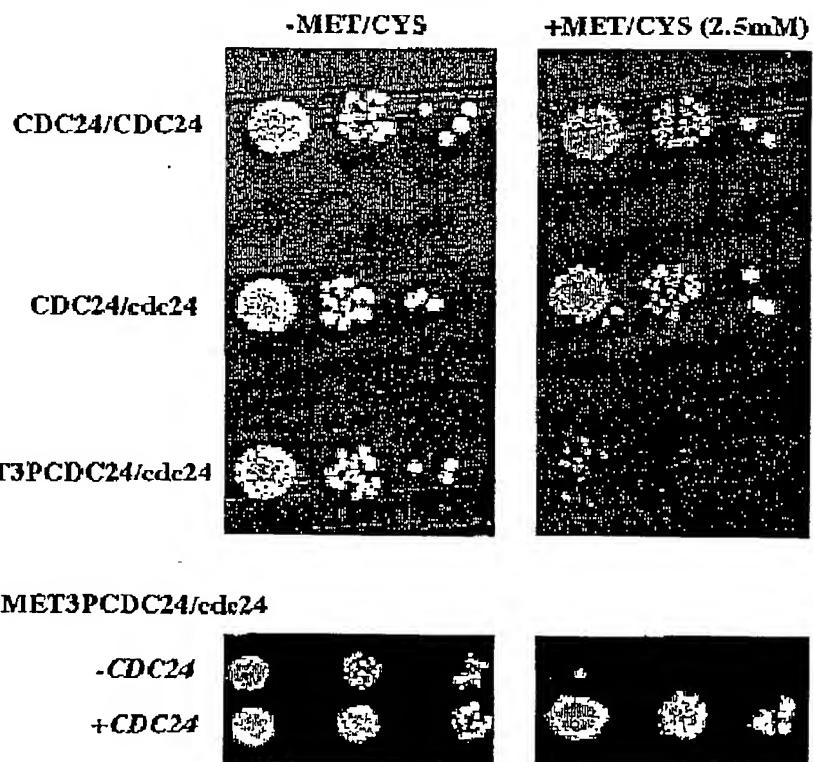
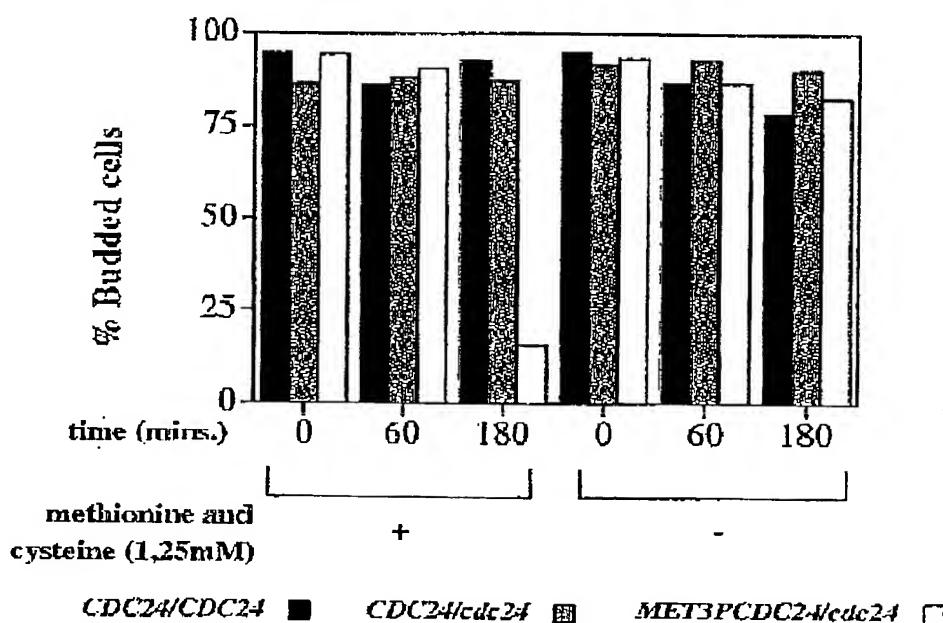
**Figure 10**

Figure 11

**A****B**

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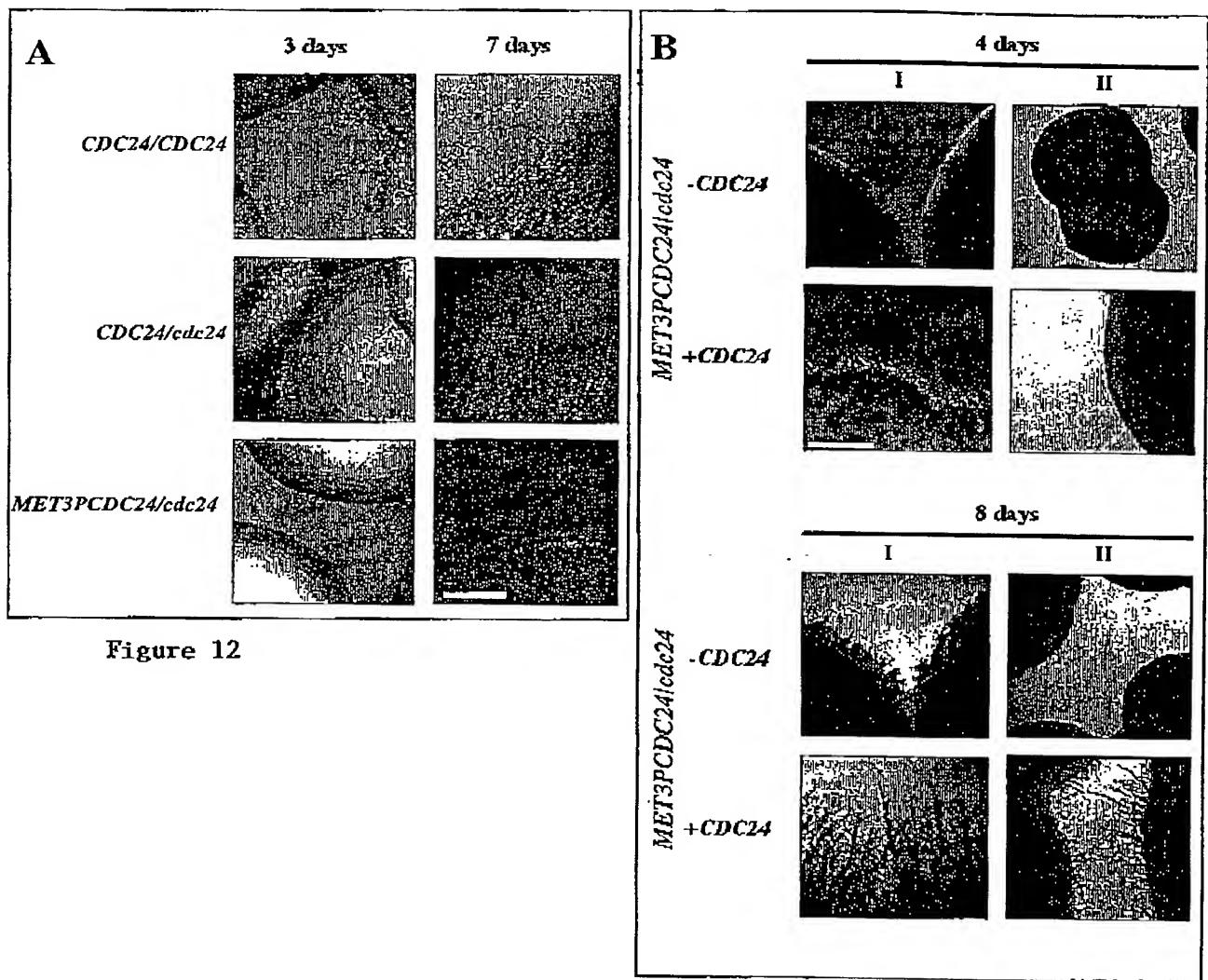
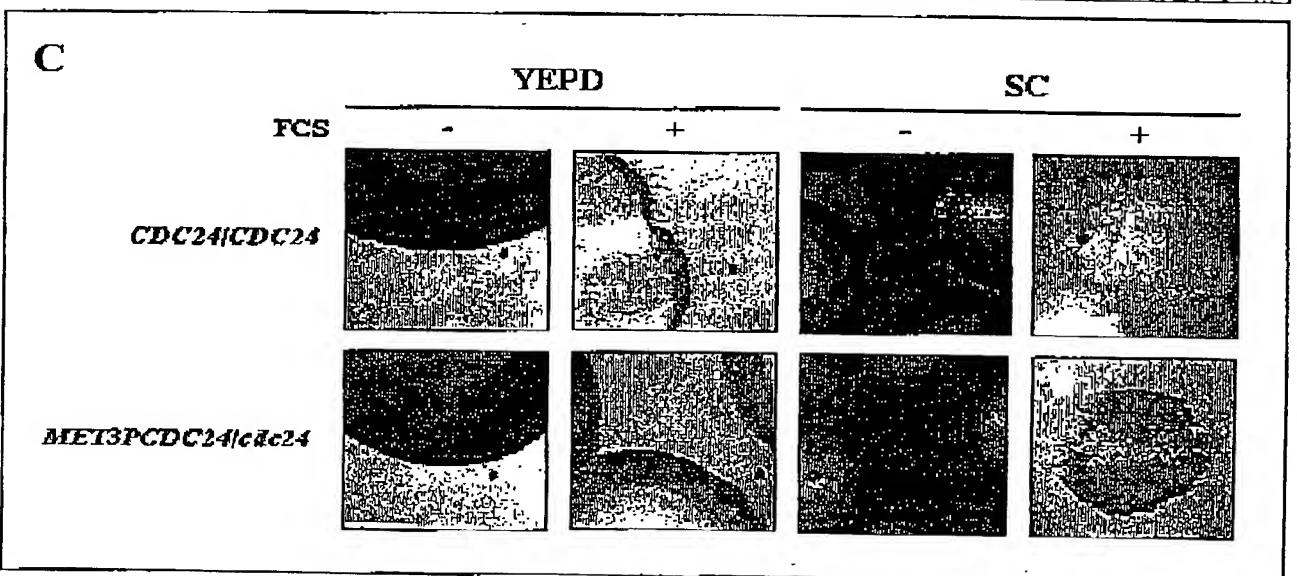


Figure 12



14A

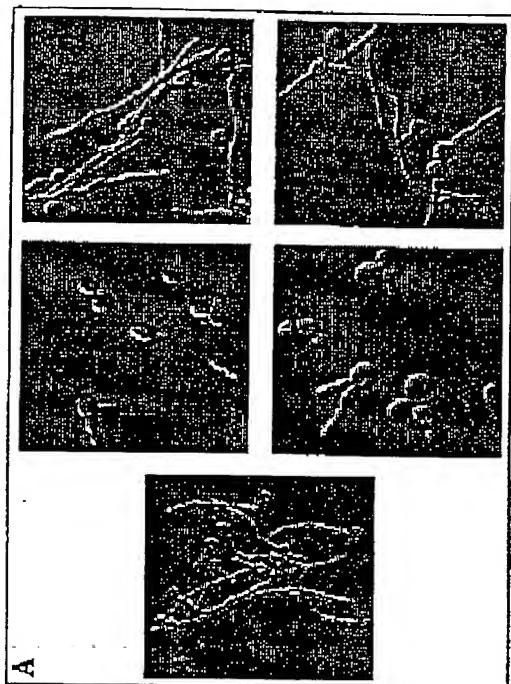
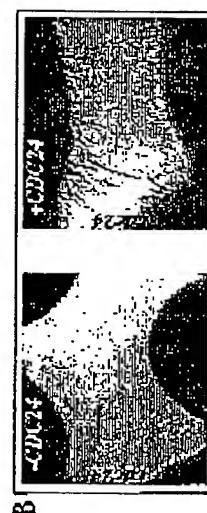
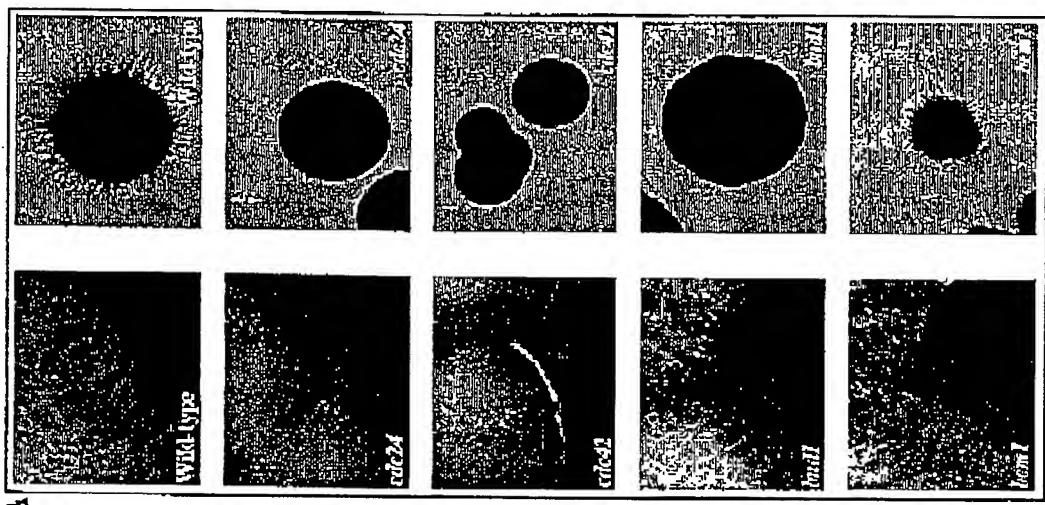


Figure 14B



Figure 13



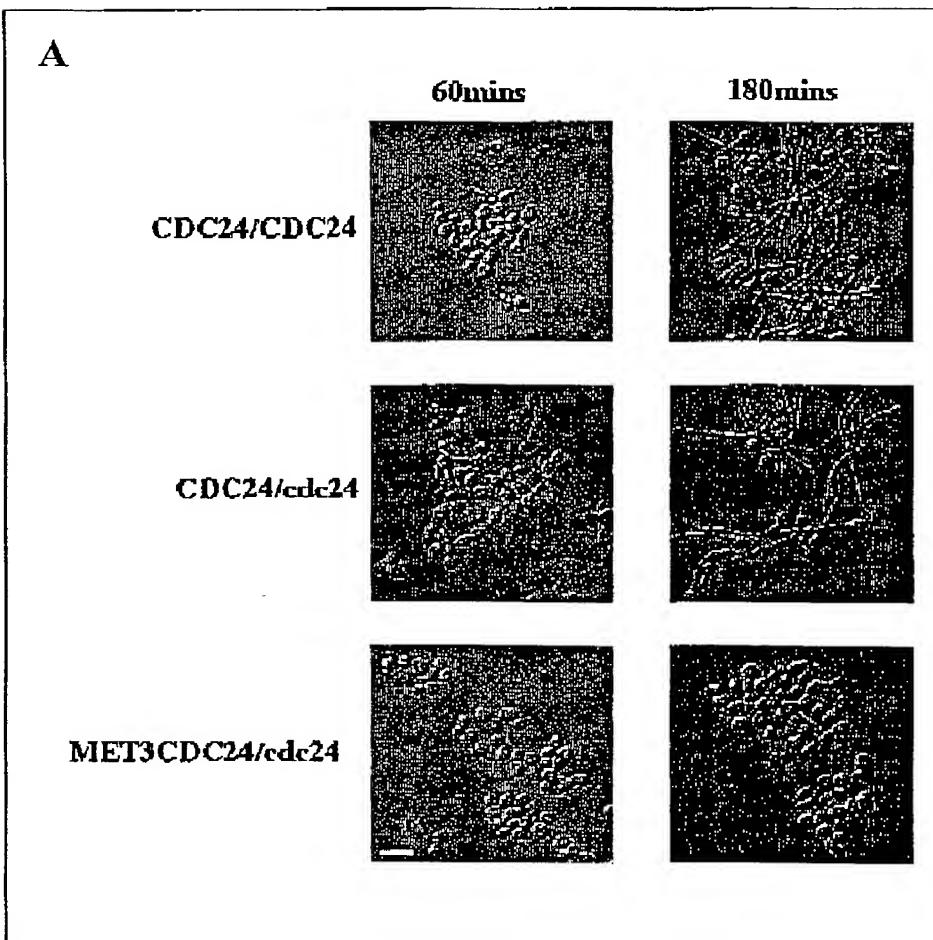


Figure 15

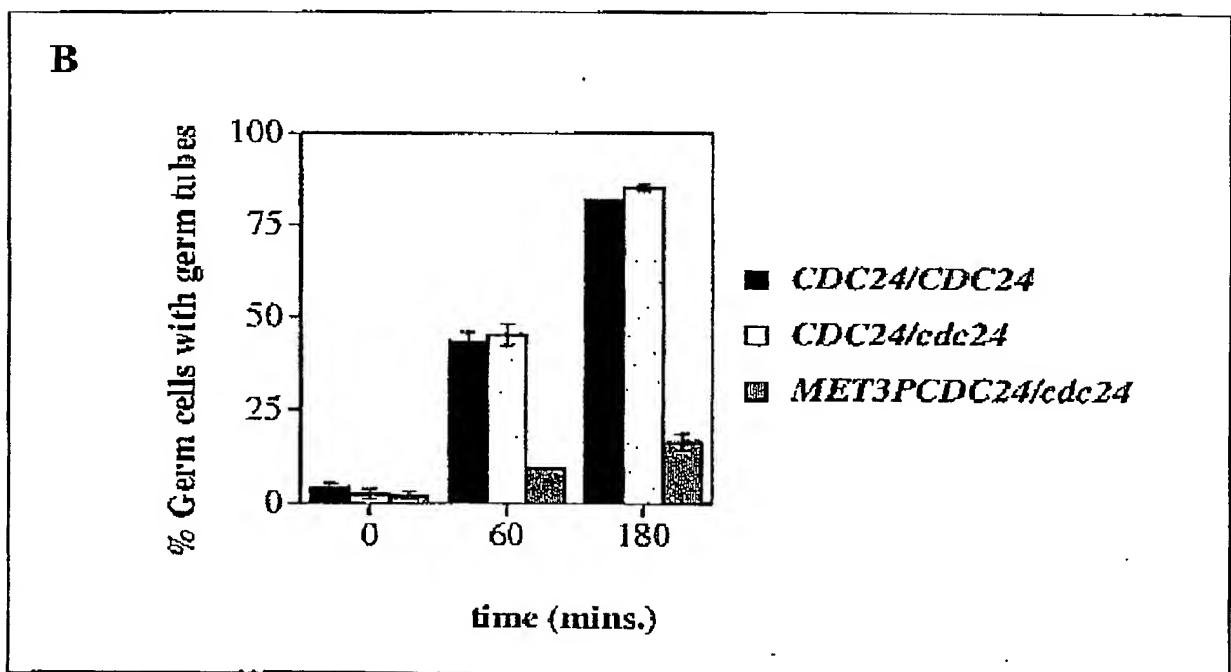


Figure 16

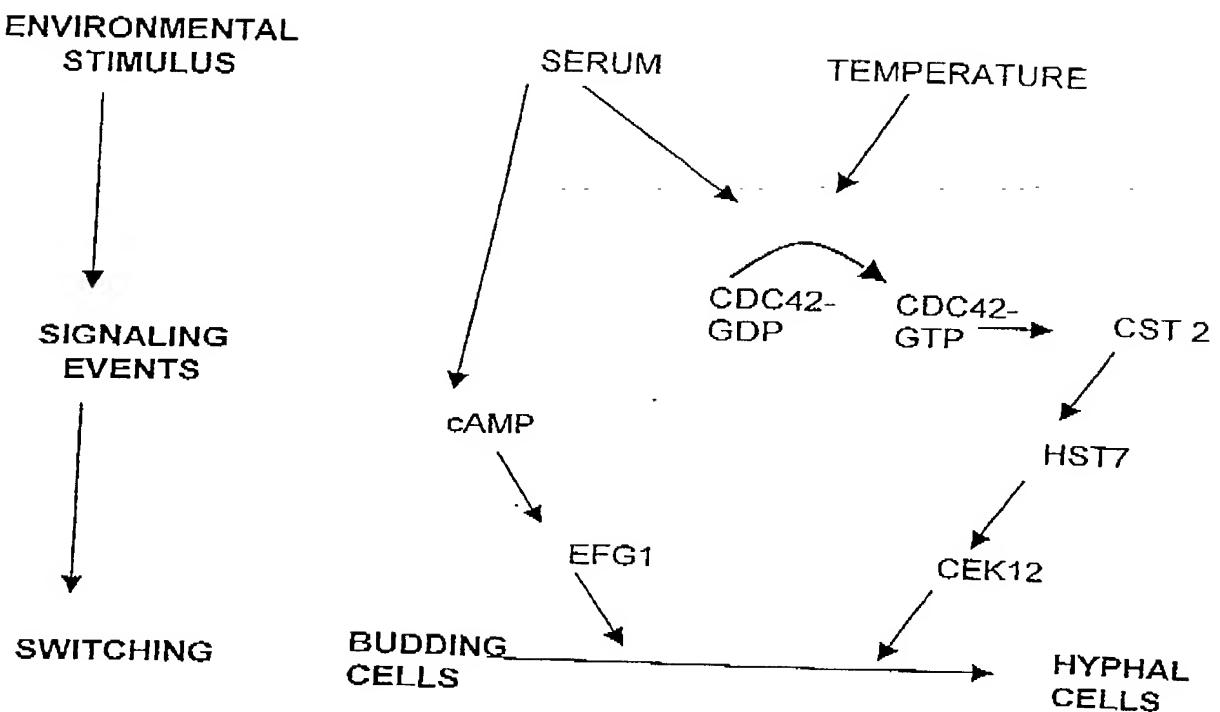


Figure 17

A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatctgacgatttgaagtcgtaaaaaaaaatccatttatgactt  
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatttgcacgatttgaagtcgtaaaaaaaaatccatttatgactt  
atattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccccctctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcatctggcgatttgc  
tatattgggctgcaagaaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccctctgtatactttcaactctgtgaagccgcaattaaattaccggtaatagcacctgacgatttgc  
tatattgggctgcaagaaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctggtcaaagt  
gctagaagttagtagaaacgctaataatccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEVETLMNSS

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## SEQ ID NO. 10

## STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATAATACAAACCCAGTCTACAGGA  
 TACCTCTGCAGTGGAGGAAGAAATTCAAAATAATAAGAGGCCGCCAGACAAAGAGTAACAGCTTATGCTCAATTAA  
 ATTAAGCAAAACACAGATAACAAGATGCAAGCTTATTCCAGATGCCAACAAAGTTACTCGTTGACCAAAATAAGATC  
 5 AACTTAAAGCCATTATCGTGTGAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCAGATTCAAAACGTAT  
 TTTGAGTGCAGTCAGATGGCTTATGCTTATATGGACAGTGCTTCAGGTTAAACAGAACGCTATTCCATTAGATT  
 CTCAATGGTTCTTCCTGCGCTATTCGCATCGAGTACTTGGTAGCAACCGCAGGATTAAACATAACTGTACCAT  
 TATAAGTTGCAAGAAAACAGAGTAGCGCAAAACGTTGCGTCAATTTCAAAGGACATACTTGCTATATTCTGACAT  
 TGTTTACAGATAACGCRCAATAATTGACAGCAAGTGGGGATATGACATGTGCTTGTGGGGATAACGAAACCAAAGA  
 10 GGTTGAGAGATAATTCTGACCAATTAGGTGATGTTTGGCATTAGCTATTCTGAAAGGCCAACTTAGAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTCATATGGGATAGCAGATCTCCGTCCTGTACAAAGCTTTA  
 CCTTAAACGAACTGTTATTATGGCACTTCGTTTTTCGAAGGGAATGTCATTCTGCAAGGAAATGACAAATGGTGG  
 TTTATATGTTGTTAAAGGTGGACTGTTCTATGGTACTTTGCTTCTTTCGAGGTTTCAAGAACGTAACCCCTTAC  
 CCTRACTTATACTGGAGCTAACTGGAGTACAATAACCCGGCACTGGCACAACACTTTAAATGAAAGCTCAAGCTATCT  
 15 AGAACACCAAGGCGTTGTTCTTAAAGGAGAGATGGTCAAALATTAGGGTCACTGGTGGAGTCACTGGTGTGCCCTCGAGT  
 TTGGTGGGGAGTATTAAAGGAGAGATGGTCAAALATTAGGGTCACTGGTGGAGTCACTGGTGTGCCCTCGAGT  
 CGAGATGGGTECTGTTATGACAGGTTCAACGGACTCAACCAATGAAATACTGGTGTCCAGGTTTCAATAG

20

## SEQ ID NO. 11

## Ste4 Protein sequence (wild-type)

MHQMDSITYNNVTCOYIQPQSLQDISAVEEEIQNKIEARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTQNKEI  
 LKPNIVLKGEMNKISDERWSRDSKRILSASQDGPMLIWDSASCLQNAIPLDSQWVLSCAIESPSTLVASAGLNNNCTI  
 25 RYSKEMRVAQXVASIEFKHTCYISDIEFTDNAHILTASGDMTCALWDIPKPKRVREYSODHLGCVIALAFPEEPNLNSSI  
 CEGSCGSDGYTYIWDERSPSAVQSFYVNDDINALREFKDGMNTVAGSDNGAINMYDLRSDCSIATFSLFRGYEEATPT  
 TIVAAANMEYNTAQSPQTLXSTSSSYLDNQGVVSIDFSASGRILMYSCTDTIGCVVWDVILKGEEV3KLEGHGGRVTGVRES  
 DGLAVCTGSWDSSTMKIEWSPGYQ

30

## SEQ ID NO. 12

## ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATAATACAAACCCAGTCTACAGGA  
 35 TACCTCTGCAGTGGAGGAAGAAATTCAAAATAATAAGAGGCCGCCAGACAAAGAGTAACAGCTTATGCTCAATTAA  
 ATTAAGCAAAACACAGATAACAAGATGCAAGCTTATTCCAGATGGCCAACAAAGTTACTTGCTTCAACAAATTAAGAT  
 AACTTAAAGCCAAATACTCGTGTGAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCAAGATTCAAAACGT

TTTGAGTCAAGTCAAGATGGCTTATGCTTATATGGACAGTGCTCAGGTTAAACAGAACGCTATTCCATTAGA  
 5 CTCATGGGTTCTTCCTGCCATCGAGTACCTGGTAGCAGCGCAGGATTAACGCTAACTGTACCAT  
 TATAGAGTTCGAAAAGAAAACAGACTAGCGAAAACGTTGCCTCAATTTCAGGACATACTTGTATATTCTGACA  
 TGAATTACAGATAACGCACATATATTGACAGCACTGGGGATATGACATGTGCCTTGTGGATATACCGAAAGCAAAG  
 10 GGGTGGAGAGGATATTCTGACCATTAGGTGATGTTGGCATTAGCTATTCCCTGAAGAGCCAACTTAGAAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGCTCGCTGACAAAGCTTT  
 CGTTAACCGATAGTGTATTAATGCACTTCGTTTCAAAGACGGGATGTCAGTTGTCAGGAAAGTGAACATGGTGCAG  
 TAAATATGTATGATTAAGGTGGACTGTTCTATTGCTACTTTCTCTTTCGAGGTTATGAAGAACGTACCCCTAC  
 CCTACTTATATGGCAGCTAACATGGACTACAATACCGCGCAATGCCACAACTTTAAATCAGCTGCTCAAGCTATC  
 15 AGACAACCAAGGCCTGTTCTTAGATTTAGTCATCTGGAAAGATTGATGACTCATGCTATACAGACATGGTTGT  
 TTGTGTGGATGTTAAAGGAGAGATTGTTGAAAGGTCACTGGTGGCAGAGTCACTGGTGTGCCTCGAG  
 CGAGATGGGTTAGCTGTATGTCAGGTTCATGGACTCACCATGAAATATGGCTCCAGGCTTCATG  
 SEQ ID No. 13

## 15 Ste4-o15 Protein sequence (mutant)

MAHQMDSITYSNNTQOYIQPQLQDISAVEEEIQNKIEARQESKQLHAIINKAKHKGQDASLFOAMANKVTSLTKNK  
 LKPNIIVLKHNKISDFRWSRDSKRILSASQDGFMILWDSASGLKQNAIPLDQSOWVLSCAISSSTLVASAGLNNNCT  
 RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTDASGDMTCALWDIPKAKRVRGYSDELGDVLAATPEEPNLENS  
 20 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSINALRFFKDGMSTIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTP  
 TYMAANMEYNTAQSPOTLKSTSSSYLDNQGVVSLDFSASGRMLMYSCYTDCIGCVVWDVLKGIVVKLEGHGGRTGVRS  
 DGLAVCTGSDSTMKIWSPGYQ

## SEQ ID NO. 14

## 25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACACACAAAGTCTACAGGA  
 TATCTCTGAGTGGAGGAAGAAATTCAATAAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATP  
 ATAAAGCTAAACACAAAGATACAAGATGCAAGCTTATCCAGATGGCCACAAAGTTACTTCGTTACCAAAATAAGAT  
 30 AACTTAAAGCCAAATATCGTGTGAAAGGCCATAATAATAAAATCTCAGATTTCGGTGGAGTCGAGATTCAAAACGTA  
 TTTGAGTCAAGTCAAGATGGCTTATGCTTATATGGACAGTGCTTCAGGTTAAACAGAACGCTATTCCATTAGAT  
 CTCAATGGTTCTTCCTGCGTATTCGCCATCGAGTACTTGGTAGCAGCGCAGGATTAAACATAACTGTACCAT  
 TATAGAGTTGCAAAACAGAGTACCGCAAAACGTTGCCTCAACTTGGAGAACAGTACTTGTATATTCTGACA  
 TGAAATTACAGATAACGCACATATATTGACAGCACTGGGGATATGACATGTGCCTTGTGGATATACCGAAAGCAAAG  
 35 GGGTGAGAGAAATTCTGACCATTAGGTGATGTTGGCATTAGCTATTCCCTGAAGAGCCAAACTTAGAAAATTCTTC  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCGTCCGCTGACAAAGCTTT  
 CGTTAACGATAGTGTATTAATGCACTTCGTTTCAAAGACGGGATGTCGATTGTCAGGAAAGTGAACATGCTGCG

TAAATATGATTAAGTCGGACTGTTCTATTGCTACTTTCTCTTTCGAGGTATGAAGAACGTACCCCTAC  
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATGCCACAAACTTAAAATCAACAAAGCTCAAGCTATCI  
 AGACAACCAAGGGCGTGTCTTAGATTTAGTGCATCTGAAAGATTGATGACTCATGCTATAACAGACATTGGTTGTC  
 TTGTGTGGATGTATTAAGGAGAGATTGGAAATTAGAAGGTATGGTGGCAGAGTCACTGGTGTGGCTCGAGI  
 5 CCAGATGGGTTAGCTGTATGTACAGGTTATGGGACTCAACCATGAAATATGGTCTCCAGGTTATCAATAG

## SEQ ID No. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSTIYSNNVTQQYIQPQLQDISAVEEEIQNKIEARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKII  
 LKPNIVLKGHNNKISDFRWSRDSKRILSASQDGFMILWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNCTI  
 RVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKPKRVREYSQHLGDVIAAIPIPEEPNLNSSI  
 TFASCSDGYTYIWDSRSRSPSAVQSFYVNDSDINALRFFKDGMSTIVAGSDNGAINMYDLRSDCSIAFSLFRGYEERTPTI  
 TYMAANMEYNTAQSPQTLKSTSSSYLDNQAVSLDFSASGRIMYSCTDYGCVVWDVLKGEIVGKLEGHGGRTGVRSEI  
 15 DGLAVCTGSWDSTMKIWSPGYQ

SEQ. I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ. I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly"

SEQ. I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ. I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ. I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ. I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ. I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKTI".